

1: AX354891. Sequence 1 from P...[gi:18619594] [Links](#)

//

May 20 2003 11:20:12



results of BLAST

BLASTX 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1053530926-012060-5027

Query=

(623 letters)

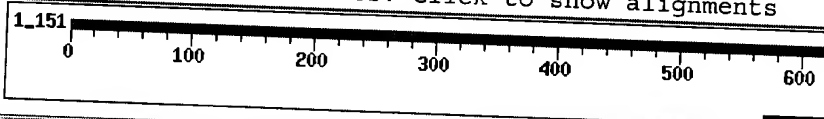
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
1,436,082 sequences; 461,603,290 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 1 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

gi|11493456|gb|AAG35502.1|AF130117 34 PRO2532 [Homo sapiens]

33 3.1

Alignments

>gi|11493456|gb|AAG35502.1|AF130117 34 PRO2532 [Homo sapiens]
Length = 71

Score = 33.1 bits (74), Expect = 3.1
Identities = 13/17 (76%), Positives = 13/17 (76%)
Frame = -3

Query: 621 CLSMFTYINSYHCVLIA 571
CL MF Y NSYHCV IA
Sbjct: 43 CLDMFRYTNSYHCVTIA 59

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
Posted date: May 21, 2003 1:35 AM
Number of letters in database: 461,603,290
Number of sequences in database: 1,436,082



results of BLAST

BLASTN 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1053530268-026904-27289

Query=

(623 letters)

DNA

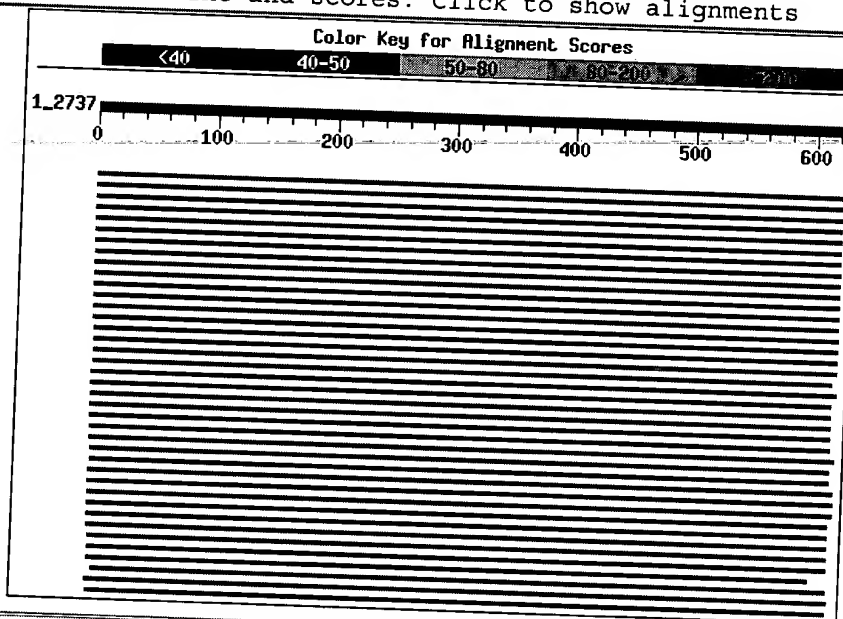
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)
1,766,999 sequences; 8,277,202,449 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 116 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

					Score (bits)	E Value
gi	25815516	gb	AC019340.6	Homo sapiens BAC clone RP11-715L...	1235	0.0
gi	22138720	gb	AC127701.2	Homo sapiens BAC clone RP11-79F1...	1235	0.0
gi	22002241	gb	AC110072.3	Homo sapiens BAC clone RP11-18C1...	1084	0.0

gi	23268261	gb	AC129782.3	Homo sapiens BAC clone RP11-2807...	1037	0.0
gi	22830260	gb	AC133485.1	Homo sapiens chromosome 16 clone...	1029	0.0
gi	4753268	gb	AC006352.3	Homo sapiens PAC clone RP5-1044J9...	1029	0.0
gi	29570354	gb	AC140873.3	Homo sapiens chromosome 16 clone...	1013	0.0
gi	29171396	gb	AC138916.3	Homo sapiens chromosome 16 clone...	1013	0.0
gi	27901832	gb	AC138815.2	Homo sapiens chromosome 16 clone...	1013	0.0
gi	27923649	gb	AC138869.2	Homo sapiens chromosome 16 clone...	1013	0.0
gi	13518279	gb	AC018696.4	Homo sapiens BAC clone RP11-575H...	1013	0.0
gi	28933522	gb	AC140890.2	Homo sapiens chromosome 16 clone...	942	0.0
gi	29501021	emb	AL031601.4	HSY237C10 Human DNA sequence fro...	926	0.0
gi	27261502	gb	AC136428.3	Homo sapiens chromosome 16 clone...	922	0.0
gi	26023960	gb	AC136877.2	Homo sapiens chromosome 16 clone...	922	0.0
gi	24416017	gb	AC127536.5	Homo sapiens chromosome 15, clon...	922	0.0
gi	19745004	gb	AC092342.3	Homo sapiens chromosome 16 clone...	922	0.0
gi	16604077	gb	AC093787.3	Homo sapiens BAC clone RP11-215P...	922	0.0
gi	29029247	gb	AC138907.2	Homo sapiens chromosome 16 clone...	912	0.0
gi	29294039	gb	AC138807.2	Homo sapiens chromosome 16 clone...	912	0.0
gi	29294003	gb	AC140899.3	Homo sapiens chromosome 16 clone...	912	0.0
gi	28261473	gb	AC137761.3	Homo sapiens chromosome 16 clone...	912	0.0
gi	25139875	gb	AC136425.3	Homo sapiens chromosome 16 clone...	912	0.0
gi	22213392	gb	AC069061.11	Homo sapiens chromosome 16 clone...	912	0.0
gi	29244707	gb	AC103582.17	Homo sapiens chromosome 17, clo...	912	0.0
gi	28261563	gb	AC138701.3	Homo sapiens chromosome 22 clon...	910	0.0
gi	23130719	gb	AC127381.4	Homo sapiens chromosome 15, clon...	908	0.0
gi	29171367	gb	AC141272.3	Homo sapiens BAC clone RP11-1360...	908	0.0
gi	29171366	gb	AC141248.2	Homo sapiens chromosome 16 clone...	904	0.0
gi	27877169	gb	AC136613.3	Homo sapiens chromosome 16 clone...	904	0.0
gi	26449052	gb	AC133536.2	Homo sapiens chromosome 16 clone...	904	0.0
gi	7622520	gb	AC007882.3	Homo sapiens chromosome 16 clone...	904	0.0
gi	6693583	gb	AC007028.3	Homo sapiens BAC clone RP11-499D5...	904	0.0
gi	22202841	dbj	AP005242.2	Homo sapiens chromosome 16 clone ...	904	0.0
gi	28872836	dbj	AP005901.2	Homo sapiens genomic DNA, chrom...	878	0.0
gi	29469645	gb	AC142121.2	Homo sapiens genomic DNA, chrom...	870	0.0
gi	23266392	gb	AC129779.2	Homo sapiens chromosome 7 clone ...	852	0.0
gi	24757127	gb	AC127389.2	Homo sapiens BAC clone RP11-1360...	850	0.0
gi	28564355	emb	AL732363.8	Homo sapiens BAC clone RP11-142N...	844	0.0
gi	27777620	gb	AC138789.1	Human DNA sequence from clone R...	844	0.0
gi	27905022	gb	AC128674.3	Homo sapiens BAC clone CTD-2593N...	837	0.0
gi	25809666	emb	AL954711.3	Homo sapiens BAC clone RP11-1390...	837	0.0
gi	18097282	gb	AC023141.6	Human DNA sequence from clone R...	837	0.0
gi	4753263	gb	AC006359.3	Homo sapiens BAC clone RP11-548K...	837	0.0
gi	24158580	gb	AC127384.4	AC006359 Homo sapiens clone DJ1135...	837	0.0
gi	18614049	emb	AL592492.10	Homo sapiens BAC clone RP11-1390...	829	0.0
gi	22002240	gb	AC127387.3	Human DNA sequence from clone ...	829	0.0
gi	19310353	gb	AC114501.1	Homo sapiens BAC clone RP11-28J3...	789	0.0
gi	29124082	gb	AC106819.3	Homo sapiens BAC clone RP11-667F...	777	0.0
gi	3873180	gb	AC005939.1	Homo sapiens chromosome 16 clone...	765	0.0
gi	18152763	emb	AL117348.26	AC005939 Homo sapiens chromosome 1...	78	2e-11
gi	14010935	gb	AC073137.7	HSDJ559A3 Human DNA sequence fr...	74	3e-10
gi	13751453	emb	AL390205.17	AC073137 Homo sapiens BAC clone R...	66	7e-08
gi	16258903	gb	AC025031.30	Human DNA sequence from clone ...	66	7e-08
gi	21954877	gb	AC110717.11	Homo sapiens 12 BAC RP11-474P2 ...	64	3e-07
gi	18449613	gb	AC073358.14	Homo sapiens 3 BAC RP11-419H8 (...)	64	3e-07
gi	11121083	emb	AL391840.6	Homo sapiens 3 BAC RP11-501M7 (...)	64	3e-07
gi	21728162	dbj	AP005209.3	Human DNA sequence from clone R...	64	3e-07
gi	24110956	gb	AC034195.7	Homo sapiens genomic DNA, chrom...	62	1e-06
gi	20128363	gb	AC105108.4	Homo sapiens chromosome 3 clone ...	60	4e-06
gi	17386235	gb	AC008934.5	Homo sapiens chromosome 8, clone...	60	4e-06
gi	16943998	emb	AL356073.15	Homo sapiens chromosome 5 clone ...	60	4e-06
gi	11323376	gb	AC023478.5	Human DNA sequence from clone ...	60	4e-06
gi	11323371	gb	AC018492.6	AC023478 Homo sapiens chromosome ...	60	4e-06
gi	4156209	gb	AC004816.1	AC018492 Homo sapiens chromosome ...	60	4e-06
gi	8272457	gb	AF131215.1	AC004816 Homo sapiens PAC clone RP...	60	4e-06
gi	2388554	gb	AC002528.1	AF131215 Homo sapiens chromosome 8...	60	4e-06
gi	21322173	gb	AC002456.2	AC002528 Human BAC clone GS1-542D1...	60	4e-06
				Homo sapiens BAC clone CTB-13L3 ...	58	2e-05

gi	19774315	gb	AC107295.4	Homo sapiens 3 BAC RP11-1E5 (Ros...	58	2e-05
gi	18997372	gb	AC079070.6	Homo sapiens chromosome 18, clon...	58	2e-05
gi	17047144	gb	AC090226.3	Homo sapiens chromosome 18, clon...	58	2e-05
gi	13397792	emb	AL109628.5	CNS0180T Human chromosome 14 DNA...	58	2e-05
gi	16151426	emb	AL392172.9	Human DNA sequence from clone R...	58	2e-05
gi	5091645	gb	AC005235.2	AC005235 Homo sapiens BAC clone RP...	58	2e-05
gi	28189493	dbj	AP002387.4	Homo sapiens genomic DNA, chrom...	58	2e-05
gi	21623946	dbj	AP000867.5	Homo sapiens genomic DNA, chrom...	58	2e-05
gi	20127999	gb	AC103895.3	Papio anubis clone RP41-397E13, ...	56	7e-05
gi	27261610	gb	AC135075.5	Homo sapiens chromosome 8, clone...	56	7e-05
gi	26348018	gb	AF129408.4	Homo sapiens chromosome 21 clone...	56	7e-05
gi	17737018	gb	AC073583.19	Homo sapiens Xp BAC RP11-483M24...	56	7e-05
gi	3659406	gb	AC005704.1	Homo sapiens X BAC GSHB-227L7 (Ge...	56	7e-05
gi	19852144	gb	AC105225.5	Homo sapiens chromosome 8, clone...	56	7e-05
gi	19747179	gb	AC114277.2	Homo sapiens chromosome 5 clone ...	56	7e-05
gi	18921230	gb	AC083803.8	Homo sapiens 3q BAC RP11-142C12 ...	56	7e-05
gi	15638764	gb	AC096557.1	Homo sapiens BAC clone RP11-122A...	56	7e-05
gi	18034740	gb	AC011092.4	Homo sapiens, clone RP11-1H15, c...	56	7e-05
gi	15668073	gb	AC096636.1	Homo sapiens chromosome 1 clone ...	56	7e-05
gi	15290355	gb	AC022113.6	Homo sapiens chromosome 5 clone ...	56	7e-05
gi	7159777	emb	AL132773.14	HSDJ741H3 Human DNA sequence fro...	56	7e-05
gi	7717362	emb	AL163279.2	HS21C079 Homo sapiens chromosome ...	56	7e-05
gi	14268331	emb	AL117356.5	CNS01DRK Human chromosome 14 DNA...	56	7e-05
gi	8176896	emb	AL049873.3	CNS0000T Human chromosome 14 DNA ...	56	7e-05
gi	13445448	emb	AL451146.7	Human DNA sequence from clone R...	56	7e-05
gi	14787305	emb	AL359736.19	Human DNA sequence from clone ...	56	7e-05
gi	15384823	emb	AL590639.9	Human DNA sequence from clone R...	56	7e-05
gi	13324813	gb	AC015599.5	AC015599 Homo sapiens chromosome ...	56	7e-05
gi	8748916	gb	AC006994.4	AC006994 Homo sapiens BAC clone RP...	56	7e-05
gi	3046306	gb	AC004549.1	AC004549 Homo sapiens BAC clone CT...	56	7e-05
gi	4508124	gb	AC006465.2	AC006465 Homo sapiens BAC clone RP...	56	7e-05
gi	5649375	gb	AC007253.2	AC007253 Homo sapiens BAC clone RP...	56	7e-05

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|25815516|gb|AC019340.6| ☒ Homo sapiens BAC clone RP11-715L17 from 7, complete
Length = 190137

Score = 1235 bits (623), Expect = 0.0
Identities = 623/623 (100%)
Strand = Plus / Minus

Query: 1 atccatataccatataagtggccatttcattttgccttcttccaccaaattcttagcaacc 60
Sbjct: 82347 atccatataccatataagtggccatttcattttgccttcttccaccaaattcttagcaacc 82288

Query: 61 tcaaccattgccatgagccactgtaggcctaccgtctacaaacaacaagtatcatttga 120
Sbjct: 82287 tcaaccattgccatgagccactgtaggcctaccgtctacaaacaacaagtatcatttga 82228

Query: 121 aaacatttcataatcccatttgataaatttcccagcaaagagatgcttactttaactcta 180
Sbjct: 82227 aaacatttcataatcccatttgataaatttcccagcaaagagatgcttactttaactcta 82168

Query: 181 tgcaagtggctcatattcgcaaagtctggagatattattcaggtagtgtgagaaaatctt 240
Sbjct: 82167 tgcaagtggctcatattcgcaaagtctggagatattattcaggtagtgtgagaaaatctt 82108

Query: 301 ccatagggttagagatttgtattttcacagtacaacaatggttatggagggtcattgaaactta 360
|||||
Sbjct: 5711 ccatagggttagagatttgtattttcacagtacaacaatggttatggagggtcattgaaactta 5770

Query: 361 gattgagcatttcagcacagtcacgcatcactgaatgacagggatacgttctaacaatg 420
|||||
Sbjct: 5771 gattgagcatttcagcacagtcacgcatcactgaatgacagggatacgttctaacaatg 5830

Query: 421 catccatagggaatttcacattttgcaaacgtcagagaaaatattacaaacacctagtt 480
|||||
Sbjct: 5831 catccatagggaatttcacattttgcaaacgtcagagaaaatattacaaacacctagtt 5890

Query: 481 tgtacagcctaccacgtttaggttatatgggtataacctctctctcctagggtacaaacct 540
|||||
Sbjct: 5891 tgtacagcctaccacgtttaggttatatgggtataacctctctctcctagggtacaaacct 5950

Query: 541 gtgtactacactactataactgaatactgcaggcaataagaacacagtggttaagagtttat 600
|||||
Sbjct: 5951 gtgtactacactactataactgaatactgcaggcaataagaacacagtggttaagagtttat 6010

Query: 601 gtatgtaaacataacttaaacata 623
|||||
Sbjct: 6011 gtatgtaaacataacttaaacata 6033

☐ >gi|22138720|gb|AC127701.2|
Length = 161405

Homo sapiens BAC clone RP11-79F18 from UL, complete

Score = 1235 bits (623), Expect = 0.0
Identities = 623/623 (100%)
Strand = Plus / Plus

Query: 1 atccatataccatataagtggccatttcattttgccttcttcaccaaactcttagcaacc 60
|||||
Sbjct: 91664 atccatataccatataagtggccatttcattttgccttcttcaccaaactcttagcaacc 91723

Query: 61 tcaaccattgccatgagccactgtaggcctaccgtctacaaacaaacaagtatcatttga 120
|||||
Sbjct: 91724 tcaaccattgccatgagccactgtaggcctaccgtctacaaacaaacaagtatcatttga 91783

Query: 121 aaacacttcataatcccatttgataaatttccagcaaagagatgcttactttaactcta 180
|||||
Sbjct: 91784 aaacacttcataatcccatttgataaatttccagcaaagagatgcttactttaactcta 91843

Query: 181 tgcaagtggctcatattcgcaaagtctggagatattattcaggtagtgagaaaaatctt 240
|||||
Sbjct: 91844 tgcaagtggctcatattcgcaaagtctggagatattattcaggtagtgagaaaaatctt 91903

Query: 241 cccagcgattccagcacattctccttcccatgatctgcttagtttgcaaacatattcagg 300
|||||
Sbjct: 91904 cccagcgattccagcacattctccttcccatgatctgcttagtttgcaaacatattcagg 91963

Query: 301 ccatagggttagagatttgtattttcacagtacaacaatggttatggagggtcattgaaactta 360

Sbjct: 91964 ccatagggttagagatttgatattcacagtacaacaatggtatggagggtcattgaaactta 92023

Query: 361 gattgagcatttcagcacagtcacgcatcactgaatgacagggatacgttctaacaatg 420

Sbjct: 92024 gattgagcatttcagcacagtcacgcatcactgaatgacagggatacgttctaacaatg 92083

Query: 421 catccatagggaatttcattttgcaaacgtcagagaaaattacaaacacctagtt 480

Sbjct: 92084 catccatagggaatttcattttgcaaacgtcagagaaaattacaaacacctagtt 92143

Query: 481 tgtacagcctaccacgtttagggttatatggtataacctctctctcctagggtacaaacct 540

Sbjct: 92144 tgtacagcctaccacgtttagggttatatggtataacctctctctcctagggtacaaacct 92203

Query: 541 gtgtactacactactataactgaatactgcaggcaataagaacacagtggttaagagtttat 600

Sbjct: 92204 gtgtactacactactataactgaatactgcaggcaataagaacacagtggttaagagtttat 92263

Query: 601 gtatgtaaacataacttaaacata 623

Sbjct: 92264 gtatgtaaacataacttaaacata 92286

Score = 868 bits (438), Expect = 0.0

Identities = 573/618 (92%)

Strand = Plus / Plus

Query: 3 ccatataccatataagtggccatttcattttgccttcttccaccaaactcttagcaacctc 62

Sbjct: 60035 ccatataccatataagtggccatttcattttgccttcttccaccaaactcttagcaacctc 60094

Query: 63 aaccattgccatgagccactgtaggcctaccgtctacaaacaacaagtatcatttgaaa 122

Sbjct: 60095 aaccattgccatgagccactgtaggcctaccagctacaaacaacaagtatcttttaaaa 60154

Query: 123 acacttcataatcccatttgataaattcccagcaaagagatgcttactttaactctatg 182

Sbjct: 60155 acacttcataatcccatttgataaattcccagcaaagagatgcttactttaaatctatg 60214

Query: 183 caagtggctcatattcgcaaagtctggagatattattcaggtagtgtagaaaaatcttcc 242

Sbjct: 60215 caagtggctcatattcacgaattctgtagatattattcatgtagtgtagaaaaatcatcc 60274

Query: 243 cagcgattccagcacattctccttcccatgatctgcttagtttgcaaacatattcaggcc 302

Sbjct: 60275 cagcgatgccagcacattctccttcccatgatctgcttagtttgcaaacatattcagcc 60334

Query: 303 atagggttagagatttgatattcacagtacaacaatggtatggagggtcattgaaacttaga 362

Sbjct: 60335 atgggtgacagatttgatattcacagtaaaacaattttatggaggacattgaaacttaga 60394

Query: 363 ttgagcatttcagcacagtcacgcatcactgaatgacagggatacgttctaacaatgca 422

Sbjct: 27007 tgtacagcctaccacgtttaggttatatggcataacctctctctcctaggtacaaactt 26948

Query: 541 gtgtactacactactataactgaatactgcaggcaataagaacacagtggtaagagtttat 600
|||||

Sbjct: 26947 gtgtactacattactataactgaatactgcaggcaataagaacacagtggtaagagtttat 26888
|||||

Query: 601 gtatgtaaactatacttaaacata 623
|||||

Sbjct: 26887 gtatgtaaactatacttaaacata 26865
|||||

☐ >gi|22830260|gb|AC133485.1| Homo sapiens chromosome 16 clone RP11-56L13, comple
Length = 183297

Score = 1029 bits (519), Expect = 0.0
Identities = 598/623 (95%), Gaps = 1/623 (0%)
Strand = Plus / Plus

Query: 1 atccatataccatataagtggccatttcattttgccttcttccaccaaactcttagcaacc 60
|||||

Sbjct: 8929 atccatataccatctaagtggccatttcattttgccttcttccaccaaactcttagcaacc 8988
|||||

Query: 61 tcaaccattgccatgagccactgtaggcctaccgtctacaaacaaacaagtatcatttga 120
|||||

Sbjct: 8989 tcaaccactgccatgagccactgtaggcctaccgtctacaaacaaacaagtatcttttaa 9048
|||||

Query: 121 aaacacttcataatcccatttgataaatttcccagcaaagagatgcttactttaactcta 180
|||||

Sbjct: 9049 aaacacttcataactccggttgataaaaattcccagcaaagagatgcttactttaactcta 9108
|||||

Query: 181 tgcaagtggctcatattcgcaaagtctggagatattattcaggtagtgtagaaaaatctt 240
|||||

Sbjct: 9109 tgcaagtggctcatattcgcaaagtctggagatattattcatgtagtgtagaaaaatcat 9168
|||||

Query: 241 cccagcgattccagcacattctccttcccatgatctgcttagtttgcaaacatattcagg 300
|||||

Sbjct: 9169 cccagcgatgccagcacattctccttcccatgatctgcttagttggcaaacacattcaga 9228
|||||

Query: 301 ccataggttagagatttgtatttcacagtacaacaatgttatggaggtcattgaaactta 360
|||||

Sbjct: 9229 ccataggtgagagatttttatttcacagtacaacaattttatggaggtcattgaaactta 9288
|||||

Query: 361 gattgagcatttcagcacagtcacgcatcactgaatgacagggatacgttctaactatg 420
|||||

Sbjct: 9289 gatttagcatttttagc-cagtcacgcatcactgaatgacagcgatacgttctaactatg 9347
|||||

Query: 421 catccataggcaatttcatttttgcaaacgtcagagaaaatattacaaacacctagtt 480
|||||

Sbjct: 9348 catccataggcaatttcatttttgcaaacgtcagagagaatattacaaacacctagat 9407
|||||

Query: 481 tgtacagcctaccacgtttaggttatatggtataacctctctctcctaggtacaaacct 540
|||||

Sbjct: 9408 tgtacagcctaccacgtttaggttatatggtataacctctctctcctaggtacaaacct 9467
|||||

Query: 541 gtgtactacactactataactgaatactgcaggcaataagaacacagtggtaagagtttat 600
|||||
Sbjct: 9468 gtgtactacattactataactgaatactgcaggcaataagaacacagtgataagagtttat 9527

Query: 601 gtatgtaaacataacttaaacata 623
|||||
Sbjct: 9528 gtatgtaaacataacttaaacata 9550

Score = 904 bits (456), Expect = 0.0
Identities = 579/620 (93%)
Strand = Plus / Minus

Query: 1 atccatataccatataagtggccatttcattttgccttcttccaccaaactcttagcaacc 60
|||||
Sbjct: 45292 atccatataccatataagtggccatctcattttgccttcttccaccaaactcttagcaacc 45233

Query: 61 tcaaccattgccatgagccactgtaggcctaccgtctacaaacaaacaagtatcatttga 120
|||||
Sbjct: 45232 tcaaccattgccatgagccactgtaggcctaccagctacaaacaaacaagtatctttaa 45173

Query: 121 aaacacttcataatcccattttgataaatttccagcaaagagatgcttactttaactcta 180
|||||
Sbjct: 45172 aaacacttcataactcccattttgataaatttccagcaaagagacgtctactttaactcta 45113

Query: 181 tgcaagtggctcatattcgcaaagtctggagatattattcaggtagtgtagaaaaatctt 240
|||||
Sbjct: 45112 tgcaagtggctcatattcacgaagtctgtagatattattcatgtagtgtagaaaaatcat 45053

Query: 241 cccagcgattccagcacattctccttcccatgatctgcttagtttgcaaacatattcagg 300
|||||
Sbjct: 45052 cccagcgatgccagcacattctccttcccatgatctgcttagtttgcaaacatattcagg 44993

Query: 301 ccatagggttagagatttgtatttcacagtacaacaatggttatggaggtcattgaaactta 360
|||||
Sbjct: 44992 ccatgggtgagagatttgtatttcacagtacaacaattttatggagggcattgaaactta 44933

Query: 361 gattgagcatttcagcacagtcacgcactgaatgacagggatacgttctaacaatag 420
|||||
Sbjct: 44932 cattgagcatttttagtacagtcacacatcactgaatgatagggatacgttttaacagatg 44873

Query: 421 catccataggcaatttcatttttgcacacgtcagagaaaatattacaaacacctagtt 480
|||||
Sbjct: 44872 tattcataggcaatttcatttttgcacacatcacagagaatattacaaacacctagat 44813

Query: 481 tgtacagcctaccacgttttaggttatatggtataacctctctccttaggctacaaacct 540
|||||
Sbjct: 44812 tgtacagcctaccacgttttaggttatatggtatagcctcttctccttaggctacaaacct 44753

Query: 541 gtgtactacactactataactgaatactgcaggcaataagaacacagtggtaagagtttat 600
|||||
Sbjct: 44752 gtgtactacattactctactgaatactgcaggcaataagagcacagtggtaagaggttat 44693

Query: 601 gtatgtaaacataacttaaac 620
 |||||
 Sbjct: 44692 gtatctaaacataacttaaac 44673

☐ >gi|4753268|gb|AC006352.3| Homo sapiens PAC clone RP5-1044J9 from 16, complete
 Length = 126149

Score = 1029 bits (519), Expect = 0.0
 Identities = 598/623 (95%), Gaps = 1/623 (0%)
 Strand = Plus / Plus

Query: 1 atccatataccatataagtggccatttcattttgccttcttccaccaaactcttagcaacc 60
 |||||
 Sbjct: 62840 atccatataccatctaaagtggccatttcattttgccttcttccaccaaactcttagcaacc 62899

Query: 61 tcaaccattgccatgagccactgtaggcctaccgtctacaaacaaacaagtatcatttga 120
 |||||
 Sbjct: 62900 tcaaccactgccatgagccactgtaggcctaccgtctacaaacaaacaagtatcttttaa 62959

Query: 121 aaacacttcataatcccatttgataaaatttccagcaaagagatgcttactttaactcta 180
 |||||
 Sbjct: 62960 aaacacttcataactcccgtttgataaaatttccagcaaagagatgcttactttaactcta 63019

Query: 181 tgcaagtggctcatattcgcaaagtctggagatattattcaggtagtgtgagaaaatctt 240
 |||||
 Sbjct: 63020 tgcaagtggctcatattcgcaaagtctggagatattattcatgtagtgtgagaaaatcat 63079

Query: 241 cccagcgattccagcacattctccttcccatgatctgcttagtttgcaaacatattcagg 300
 |||||
 Sbjct: 63080 cccagcgatgccagcacattctccttcccatgatctgcttagttggcaaacacattcaga 63139

Query: 301 ccatagggttagagattttgtatttcacagtacaacaatgttatggaggtcattgaaactta 360
 |||||
 Sbjct: 63140 ccatagggtgagagatttttatttcacagtacaacaattttatggaggtcattgaaactta 63199

Query: 361 gattgagcatttcagcacagtcacgcacactgaatgacagggatacgttctaacaatag 420
 |||||
 Sbjct: 63200 gatttagcatttttagc-cagtcacgcacactgaatgacagcgatacgttctaacagatg 63258

Query: 421 catccataggcaatttcacattttgcaaacgtcagagaaaatattacaaacacctagtt 480
 |||||
 Sbjct: 63259 catccataggcaatttcacattttgcaaacgtcagagagaaatattacaaacacctagat 63318

Query: 481 tgtacagcctaccacgttttaggttatatggtataacctctctctccttaggctacaaacct 540
 |||||
 Sbjct: 63319 tgtacagcctaccacgttttaggttatatggtataacctctctctccttaggctacaaacct 63378

Query: 541 gtgtactacactactatactgaatactgcaggcaataagaacacagtggttaagagtttat 600
 |||||
 Sbjct: 63379 gtgtactacattactatactgaatactgcaggcaataagaacacagtgataagagtttat 63438

Query: 601 gtatgtaaacataacttaaacata 623
 |||||
 Sbjct: 63439 gtatgtaaacataacttaaacata 63461

5/21/03 11:24 AM

Identities = 596/623 (95%), Gaps = 1/623 (0%)
Strand = Plus / Minus

Query: 1 atccatataccatataagtggccatttcattttgccttcttccaccaaattcttagcaacc 60
Sbjct: 92364 atccatataccatctaagtggccatttcattttgccttcttccaccaaattcttagcaacc 92305

Query: 61 tcaaccattgccatgagccactgtaggcctaccgtctacaaacaaacaagtatcatttga 120
Sbjct: 92304 tcaaccattgccatgagccactgtaggcctaccagctacaaacaaacaagtatcttttaa 92245

Query: 121 aaacacttcataatcccatttgataaatttcccagcaaagagatgcttactttaactcta 180
Sbjct: 92244 aaacacttcataactcccgtttgataaaatttcccagcaaagagatgcttactttaactcta 92185

Query: 181 tgcaagtggctcatattcgcaaagtctggagatattattcaggtagtgtgagaaaatctt 240
Sbjct: 92184 tgcaagtggctcatattcgcaaagtctggagatattattcatgtagtgtgagaaaatcat 92125

Query: 241 cccagcgattccagcacattctccttcccatgatctgcttagtttgcaaacatattcagg 300
Sbjct: 92124 cccagcgatgccagcacattctccttcccatgatctgcttagtttgcaaacacattcaga 92065

Query: 301 ccatagggttagagatttgtatttccacagtacaacaatgttatggagggtcattgaaactta 360
Sbjct: 92064 ccatagggtgagagatttttatttccacagtacaacaatgttatggagggtcattgaaactta 92005

Query: 361 gattgagcatttccagcacagtcacgcatcactgaatgacagggatacgttctaactatg 420
Sbjct: 92004 gatttagcatttttagc-cagtcacgcatcactgaatgacagcgatacgttctaactagatg 91946

Query: 421 catccatagggaatttcatcattttgcaaacgtcagagaaaatattacaaacacctagtt 480
Sbjct: 91945 catccatagggaatttcatcattttgcaaacatcacagagaatattacaaacacctagat 91886

Query: 481 tgtacagcctaccacgttttaggttatatggtataacctctctctcctagggtacaaacct 540
Sbjct: 91885 tgtacagcctaccacgttttaggttatatggtataacctctctctcctagggtacaaacct 91826

Query: 541 gtgtactacactactataactgaatactgcaggcaataagaacacagtggttaagagtttat 600
Sbjct: 91825 gtgtactacattactataactgaatactgcaggcaataagaacacagtggttaagagtttat 91766

Query: 601 gtatgtaaacataacttaaacata 623
Sbjct: 91765 gtatgtaaacataacttaaacata 91743

Score = 912 bits (460), Expect = 0.0
Identities = 580/620 (93%)
Strand = Plus / Plus

Query: 1 atccatataccatataagtggccatttcattttgccttcttccaccaaattcttagcaacc 60

Sbjct: 56200 atccatataccatataagtggccatctcattttgccttctccaccaaactcttagcaacc 56259

Query: 61 tcaaccattgccatgagccactgtaggcctaccgtctacaaacaaacaagtatcatttga 120

Sbjct: 56260 tcaaccattgccatgagccactgtaggcctaccagctacaaacaaacaagtatcttgtaa 56319

Query: 121 aaacacttcataatcccatttgataaatttcccagcaaagagatgcttactttaactcta 180

Sbjct: 56320 aaacacttcataactcccatttgataaatttcccagcaaagagatgtctactttaactcta 56379

Query: 181 tgcaagtggctcatattcgcaaagtctggagatattattcaggtagtgtgagaaaatctt 240

Sbjct: 56380 tgcaagtggctcatattcacgaagtctgtagatattattcatgtagtgtgagaaaatcat 56439

Query: 241 cccagcgattccagcacattctccttcccatgatctgcttagtttgcaaacatattcagg 300

Sbjct: 56440 cccagcgatgccagcacattctccttcccatgatctgcttagtttgcaaacatattcagg 56499

Query: 301 ccatagggttagagatttgtatttcacagtacaacaatggttatggaggtcattgaaactta 360

Sbjct: 56500 ccatgggtgagagatttgtatttcacagtacaacaattttatggagggtcattgaaactta 56559

Query: 361 gattgagcatttcagcacagtcacgcactgaatgacagggatacgttctaacaatg 420

Sbjct: 56560 cattgagcatttttagtacagtcacacatcactgaatgatagggtacgttttaacagatg 56619

Query: 421 catccataggcaatttcattttgcaaacgtcagagaaaatattacaaacacctagtt 480

Sbjct: 56620 tattcataggcaatttcattttgcaaacatcacagagaatattacaaacacctagat 56679

Query: 481 tgtacagcctaccacgttttaggttatatggtataacctctctctcctagggtacaaact 540

Sbjct: 56680 tgtacagcctaccacgttttaggttatatggtatagcctctttctcctagggtacaaact 56739

Query: 541 gtgtactacactactataactgaatactgcaggcaataagaacacagtggttaagagtttat 600

Sbjct: 56740 gtgtactacattactctactgaatactgcaggcaataagagcacagtggttaagagtttat 56799

Query: 601 gtatgtaaactactttaaac 620

Sbjct: 56800 gtatctaaactactttaaac 56819

☐ >gi|29171396|gb|AC138916.3|
Length = 210885

Homo sapiens chromosome 16 clone RP11-629J1, comple

Score = 1013 bits (511), Expect = 0.0
Identities = 596/623 (95%), Gaps = 1/623 (0%)
Strand = Plus / Minus

Query: 1 atccatataccatataagtggccatttcattttgccttcttccaccaaactcttagcaacc 60

Sbjct: 171217 atccatataccatctagtggccatttcattttgccttcttccaccaaactcttagcaacc 171158